In the Claims

Please amend the following claims according to the following listing of claims under 37 CFR 1.121.

Listing of Claims under 37 CFR 1.121:

We claim:

1-90 (CANCELED)

91. (CURRENTLY AMENDED): A composition for use in obtaining genotype data or sample allele frequency data, comprising: one or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers, wherein the set of oligonucleotides is selected for the set's utility to determine genotype data or sample allele frequency data for each of the two or more covering markers, wherein the group of covering markers is chosen so that a CL-F region is ~~systematically covered~~ N covered to within [x, y] by the covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to 1 million base pairs and y is less than or equal to 0.2, N is an integer greater than or equal to 1, wherein N is less than maximal, whereby the number and distribution of known markers in the neighborhood of the CL-F region make it possible for N to be a greater value, the covering markers and the CL-F region being for a species of creatures, the CL-F region being a collection of one or more points on a two-dimensional CL-F map that is similar to an x-y graph, the CL-F map having the two orthogonal dimensions of chromosomal location (CL) and least common allele frequency (F), whereby each point in the region is within the distance [x, y] of each of N or more of the covering markers, ~~wherein the group of covering markers comprises thousands of bi-allelic markers,~~

wherein the CL-F region is a segment-subrange, whereby the segment-subrange is a rectangular region on the CL-F map, whereby the segment-subrange is bounded by a chromosomal segment and a least common allele frequency subrange, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome 21, whereby the length of the segment is greater than or equal to about 47 million base pairs, wherein the subrange of the segment-subrange includes the least common allele frequency 0.1,

whereby ~~wherein~~ there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.3 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

92. (CURRENTLY AMENDED): A composition as in claim 91, wherein each oligonucleotide in the set is a type (1) complementary oligoncucleotide or wherein each oligonucleotide in the set is a type (2) complementary oligonucleotide, wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics~~, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to about D_{CL} or the equivalent thereof and y is less than or equal to about 0.2, D_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1~~.

93. (CURRENTLY AMENDED): A composition as in claim 92, ~~wherein x is less than about D_{CL},~~ wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific and each covering marker is an SNP.

94-103 (CANCELED)

104. (CURRENTLY AMENDED): A composition as in claim 93, ~~95, wherein the CL-F region is a segment-subrange, wherein the segment of the segment-subrange is a segment of a chromosome and the length of the chromosome segment is equal to the length of the chromosome and~~ wherein the subrange of the segment-subrange is the subrange 0 to 0.5, ~~whereby the segment-subrange is a rectangular CL-F region that is bounded by the segment and the subrange.~~ whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

105. (CURRENTLY AMENDED): A composition as in claim ~~104, wherein x is less than or equal to 250,000 base pairs.~~ 93, wherein the subrange of the segment-subrange is the subrange 0.1 to 0.2.

106-107 (CANCELED)

108. (CURRENTLY AMENDED): A composition as in claim 93, ~~95, wherein the CL-F region is a segment-subrange, wherein the segment of the segment-subrange is a segment of a chromosome and the length of the chromosome segment is equal to the length of the chromosome and~~ wherein the subrange of the segment-subrange is the subrange 0 to ~~less than~~ 0.1, ~~whereby the segment-subrange is a rectangular CL-F region that is bounded by the segment and the subrange~~ whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

109. (CURRENTLY AMENDED): A composition as in claim 108, wherein x is less than or equal to 250,000 base pairs, whereby there are at least about 96 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every five hundred thousand base pairs.

110-166 (CANCELED)

167. (NEW): A composition as in claim 108, wherein y is 0.1, whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

168. (NEW): A composition as in claim 109, wherein N is greater than 2, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

169. (NEW): A composition as in claim 167, wherein x is less than or equal to 250,000 base pairs, whereby there are at least about 96 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every five hundred thousand base pairs.

170. (NEW): A composition as in claim 169, wherein N is greater than 2, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

171. (NEW): A composition as in claim 93, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

172. (NEW): A composition as in claim 105, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

173. (NEW): A composition as in claim 108, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

174. (NEW): A composition as in claim 109, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

175. (NEW): A composition as in claim 167, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

176. (NEW): A composition as in claim 168, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

177. (NEW): A composition as in claim 169, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

178. (NEW): A composition as in claim 170, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

179. (NEW): A composition as in claim 178, wherein the species is not human.

180. (NEW): A composition as in claim 179, wherein the species is an animal species, wherein each oligonucleotide in the set is not a 15 nucleotide oligomer, whereby each of one or more oligonucleotides in the set is not a 15 nucleotide oligomer.

181. (NEW): A composition as in claim 179, wherein the species is a plant species, wherein each oligonucleotide in the set is not a 15 nucleotide oligomer, whereby each of one or more oligonucleotides in the set is not a 15 nucleotide oligomer.

182. (NEW): A composition as in claim 108, wherein N is greater than 2, x is less than or equal to about 250,000 base pairs and y is less than or equal to about 0.1, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to about 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

183. (NEW): A composition as in claim 182, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

184. (NEW): A composition as in claim 182, wherein each oligonucleotide in the set is not a 15 nucleotide oligomer, whereby each of one or more oligonucleotides in the set is not a 15 nucleotide oligomer.

185. (NEW): A composition as in claim 170, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome number 6, whereby the length of the segment is greater than or equal to about 171 million base pairs, whereby there are at least about 1037 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

186. (NEW): A composition as in claim 182, wherein wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

187. (NEW): A composition as in claim 109, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

188. (NEW): A composition as in claim 168, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

189. (NEW): A composition as in claim 170, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

190. (NEW): A composition as in claim 174, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

191. (NEW): A composition as in claim 176, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

192. (NEW): A composition as in claim 178, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

193. (NEW): A composition as in claim 183, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

194. (NEW): A composition as in claim 184, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

195. (NEW): A composition as in claim 185, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

196. (NEW): A composition as in claim 192, wherein each oligonucleotide in the set is a 15 nucleotide oligomer.

197. (NEW): A composition as in claim 195, wherein each oligonucleotide in the set is a 15 nucleotide oligomer.

198. (NEW): A composition as in claim 192, wherein each oligonucleotide in the set is not a 15 nucleotide oligomer, whereby each of one or more oligonucleotides in the set is not a 15 nucleotide oligomer.

199. (NEW): A composition as in claim 195, wherein each oligonucleotide in the set is not a 15 nucleotide oligomer, whereby each of one or more oligonucleotides in the set is not a 15 nucleotide oligomer.

200. (NEW): A composition as in claim 199, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

201. (NEW): A composition as in claim 93, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition or wherein the apparatus comprises a glass slide and the oligonucleotides comprised in the composition are attached to the glass slide; or wherein the apparatus comprises a silicon chip and the oligonucleotides comprised in the composition are attached to the silicon chip.

202. (NEW): A composition as in claim 170, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

203. (NEW): A composition as in claim 178, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

204. (NEW): A composition as in claim 189, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

205. (NEW): A composition as in claim 192, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

206. (NEW): A composition as in claim 195, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

207. (NEW): A composition as in claim 196, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

208. (NEW): A composition as in claim 197, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.

209. (NEW): A composition as in claim 198, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.
210. (NEW): A composition as in claim 199, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.
211. (NEW): A composition as in claim 200, wherein the composition comprises copies of the set of oligonucleotides, wherein an apparatus comprises a high-density oligonucleotide array and the array comprises the composition.
212. (NEW): A composition as in claim 92, wherein each covering marker is an SNP, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction when oligonucleotides of the composition hybridize with one or more complementary alleles of one or more of the covering markers.
213 (NEW): A composition as in claim 212, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.
214 (NEW): A composition as in claim 213, wherein the chosen group of covering markers includes thousands of bi-allelic markers.
215. (NEW): A composition as in claim 212, wherein the subrange of the segment-subrange is the subrange 0 to 0.1, wherein N is greater than 2, wherein x is less than or equal to 250,000 base pairs, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

216. (NEW): A composition as in claim 215, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

217. (NEW): A composition as in claim 215, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

218. (NEW): A composition as in claim 216, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

219. (NEW): A composition as in claim 212, wherein the subrange of the segment-subrange is the subrange 0 to 0.1, wherein N is greater than 2, wherein x is less than or equal to 250,000 base pairs, wherein y is 0.1, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

220. (NEW): A composition as in claim 219, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

221. (NEW): A composition as in claim 219, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

222. (NEW): A composition as in claim 220, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

223. (NEW): A composition as in claim 221, wherein the species is not human.

224. (NEW): A composition as in claim 223, wherein the species is a plant species, wherein the signal includes a dye color, wherein the dye that produces the dye color is a HEX fluorescent dye.

225. (NEW): A composition as in 220, wherein the signal includes a dye color, wherein the dye that produces the dye color is a HEX fluorescent dye.

226. (NEW): A composition as in 220, wherein the dye that produces the dye color is a TET fluorescent dye.

227. (NEW): A composition as in 222, wherein the signal includes a dye color, wherein the dye that produces the dye color is a HEX fluorescent dye.

228. (NEW): A composition as in 222, wherein the dye that produces the dye color is a TET fluorescent dye.

229. (NEW): A composition as in 224, wherein the signal includes a dye color, wherein the dye that produces the dye color is a HEX fluorescent dye.

230. (NEW): A composition as in 224, wherein the signal includes a dye color, wherein the dye that produces the dye color is a HEX fluorescent dye.

231. (NEW): A composition as in 220, wherein the signal does not include a dye color.

232. (NEW): A composition as in 222, wherein the signal does not include a dye color.

233. (NEW): A composition as in 224, wherein the signal does not include a dye color.

234. (NEW): A composition as in claim 228, wherein the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange that is the CL-F region is the length of the entire human chromosome, wherein the length of the entire human chromosome is greater than or equal to the length of human chromosome number 6, whereby the length of human chromosome number 6 is at or about 171 million base pairs long, whereby there are at least about 1037 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

235. (NEW): A composition as in claim 214, wherein N is greater than 2, x is less than or equal to about 250,000 base pairs and y is less than or equal to about 0.1, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to about 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.